

PCT09

RAW SEQUENCE LISTING

DATE: 09/24/2001

PATENT APPLICATION: US/09/830,506

TIME: 16:26:48

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\09242001\I830506.raw

3 <110> APPLICANT: Genzyme Corporation
5 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
6 AND TREATING POLYCYSTIC KIDNEY DISEASE
9 <130> FILE REFERENCE: 126881206140
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/830,506
C--> 12 <141> CURRENT FILING DATE: 2001-08-10
14 <150> PRIOR APPLICATION NUMBER: 60/105,731
15 <151> PRIOR FILING DATE: 1998-10-28
17 <150> PRIOR APPLICATION NUMBER: 60/105,876
18 <151> PRIOR FILING DATE: 1998-10-27
20 <150> PRIOR APPLICATION NUMBER: 60/141,175
21 <151> PRIOR FILING DATE: 1999-06-25
23 <160> NUMBER OF SEQ ID NOS: 3
25 <170> SOFTWARE: FastSEQ for Windows Version 3.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 14060
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (135)...(13040)
36 <221> NAME/KEY: misc_feature
37 <222> LOCATION: (2621)...(2710)
38 <223> OTHER INFORMATION: epitope in the loop region of the polycystin
39 transmembrane domain
41 <221> NAME/KEY: misc_feature
42 <222> LOCATION: (2734)...(3094)
43 <223> OTHER INFORMATION: epitope in the loop region of the polycystin
44 transmembrane domain
46 <221> NAME/KEY: misc_feature
47 <222> LOCATION: (3166)...(3300)
48 <223> OTHER INFORMATION: epitope in the loop region of the polycystin
49 transmembrane domain
51 <221> NAME/KEY: misc_feature
52 <222> LOCATION: (3364)...(3578)
53 <223> OTHER INFORMATION: epitope in the loop region of the polycystin
54 transmembrane domain
56 <221> NAME/KEY: misc_feature
57 <222> LOCATION: (3623)...(3688)
58 <223> OTHER INFORMATION: epitope in the loop region of the polycystin
59 transmembrane domain
61 <221> NAME/KEY: misc_feature
62 <222> LOCATION: (3710)...(3914)
63 <223> OTHER INFORMATION: epitope in the loop region of the polycystin
64 transmembrane domain
66 <221> NAME/KEY: misc_feature
67 <222> LOCATION: (3931)...(4046)

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68 <223> OTHER INFORMATION: epitope in the loop region of the polycystin
69     transmembrane domain
71 <221> NAME/KEY: misc_feature
72 <222> LOCATION: (2166)...(2599)
73 <223> OTHER INFORMATION: epitope outside the loop region but within the
74     polycystin transmembrane domain
76 <221> NAME/KEY: misc_feature
77 <222> LOCATION: (4097)...(4302)
78 <223> OTHER INFORMATION: epitope in the loop region of the polycystin
79     transmembrane domain
81 <221> NAME/KEY: misc_feature
82 <222> LOCATION: (4148)...(4219)
83 <223> OTHER INFORMATION: epitope in the loop region of the polycystin
84     transmembrane domain
86 <221> NAME/KEY: misc_feature
87 <222> LOCATION: (4220)...(4302)
88 <223> OTHER INFORMATION: epitope in the loop region of the polycystin
89     transmembrane domain
91 <221> NAME/KEY: misc_feature
92 <222> LOCATION: (27)...(360)
93 <223> OTHER INFORMATION: epitope in the loop region of the polycystin
94     transmembrane domain
96 <221> NAME/KEY: misc_feature
97 <222> LOCATION: (843)...(1200)
98 <223> OTHER INFORMATION: Ig-like domain of polycystin
100 <221> NAME/KEY: misc_feature
101 <222> LOCATION: (1205)...(1625)
102 <223> OTHER INFORMATION: Ig-like domain of polycystin
104 <221> NAME/KEY: misc_feature
105 <222> LOCATION: (1626)...(2136)
106 <223> OTHER INFORMATION: Ig-like domain of polycystin
108 <221> NAME/KEY: misc_feature
109 <222> LOCATION: (2166)...(2599)
110 <223> OTHER INFORMATION: isolated polypeptide
112 <400> SEQUENCE: 1
113 gctcagcagc aggtcgcggc cgcagcccca tccagcccgc gcccgccatg ccgtccgcgg      60
114 gccccgcctg agctgcggtc tccgcgcgcg ggcgggctg gggacggcgg ggccatgcgc      120
115 gcgctgccct aacg atg ccg ccc gcc gcg ccc gcc cgc ctg gcg ctg gcc      170
116             Met Pro Pro Ala Ala Pro Ala Arg Leu Ala Leu Ala
117             1             5             10
119 ctg ggc ctg ggc ctg tgg ctc ggg gcg ctg gcg ggg ggc ccc ggg cgc      218
120 Leu Gly Leu Gly Leu Trp Leu Gly Ala Leu Ala Gly Gly Pro Gly Arg
121             15             20             25
123 ggc tgc ggg ccc tgc gag ccc ccc tgc ctc tgc ggc cca gcg ccc ggc      266
124 Gly Cys Gly Pro Cys Glu Pro Pro Cys Leu Cys Gly Pro Ala Pro Gly
125             30             35             40
127 gcc gcc tgc cgc gtc aac tgc tcg ggc cgc ggg ctg cgg acg ctc ggt      314
128 Ala Ala Cys Arg Val Asn Cys Ser Gly Arg Gly Leu Arg Thr Leu Gly
129             45             50             55             60

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131	ccc	gcg	ctg	cgc	atc	ccc	gcg	gac	gcc	aca	gcg	cta	gac	gtc	tcc	cac	362
132	Pro	Ala	Leu	Arg	Ile	Pro	Ala	Asp	Ala	Thr	Ala	Leu	Asp	Val	Ser	His	
133				65					70						75		
135	aac	ctg	ctc	cgg	gcg	ctg	gac	gtt	ggg	ctc	ctg	gcg	aac	ctc	tcg	gcg	410
136	Asn	Leu	Leu	Arg	Ala	Leu	Asp	Val	Gly	Leu	Leu	Ala	Asn	Leu	Ser	Ala	
137				80					85					90			
139	ctg	gca	gag	ctg	gat	ata	agc	aac	aac	aag	att	tct	acg	tta	gaa	gaa	458
140	Leu	Ala	Glu	Leu	Asp	Ile	Ser	Asn	Asn	Lys	Ile	Ser	Thr	Leu	Glu	Glu	
141			95					100					105				
143	gga	ata	ttt	gct	aat	tta	ttt	aat	tta	agt	gaa	ata	aac	ctg	agt	ggg	506
144	Gly	Ile	Phe	Ala	Asn	Leu	Phe	Asn	Leu	Ser	Glu	Ile	Asn	Leu	Ser	Gly	
145		110					115				120						
147	aac	ccg	ttt	gag	tgt	gac	tgt	ggc	ctg	gcg	tgg	ctg	ccg	cga	tgg	gcg	554
148	Asn	Pro	Phe	Glu	Cys	Asp	Cys	Gly	Leu	Ala	Trp	Leu	Pro	Arg	Trp	Ala	
149	125				130					135					140		
151	gag	gag	cag	cag	gtg	cgg	gtg	gtg	cag	ccc	gag	gca	gcc	acg	tgt	gct	602
152	Glu	Glu	Gln	Gln	Val	Arg	Val	Val	Gln	Pro	Glu	Ala	Ala	Thr	Cys	Ala	
153				145					150					155			
155	ggg	cct	ggc	tcc	ctg	gct	ggc	cag	cct	ctg	ctt	ggc	atc	ccc	ttg	ctg	650
156	Gly	Pro	Gly	Ser	Leu	Ala	Gly	Gln	Pro	Leu	Leu	Gly	Ile	Pro	Leu	Leu	
157			160					165				170					
159	gac	agt	ggc	tgt	ggt	gag	gag	tat	gtc	gcc	tgc	ctc	cct	gac	aac	agc	698
160	Asp	Ser	Gly	Cys	Gly	Glu	Glu	Tyr	Val	Ala	Cys	Leu	Pro	Asp	Asn	Ser	
161			175					180				185					
163	tca	ggc	acc	gtg	gca	gca	gtg	tcc	ttt	tca	gct	gcc	cac	gaa	ggc	ctg	746
164	Ser	Gly	Thr	Val	Ala	Ala	Val	Ser	Phe	Ser	Ala	Ala	His	Glu	Gly	Leu	
165		190					195				200						
167	ctt	cag	cca	gag	gcc	tgc	agc	gcc	ttc	tgc	ttc	tcc	acc	ggc	cag	ggc	794
168	Leu	Gln	Pro	Glu	Ala	Cys	Ser	Ala	Phe	Cys	Phe	Ser	Thr	Gly	Gln	Gly	
169	205				210					215					220		
171	ctc	gca	gcc	ctc	tcg	gag	ggc	tgg	tgc	ctg	tgt	ggg	gcg	gcc	cag		842
172	Leu	Ala	Ala	Leu	Ser	Glu	Gln	Gly	Trp	Cys	Leu	Cys	Gly	Ala	Ala	Gln	
173				225				230					235				
175	ccc	tcc	agt	gcc	tcc	ttt	gcc	tgc	ctg	tcc	ctc	tgc	tcc	ggc	ccc	ccg	890
176	Pro	Ser	Ser	Ala	Ser	Phe	Ala	Cys	Leu	Ser	Leu	Cys	Ser	Gly	Pro	Pro	
177			240					245				250					
179	cca	cct	cct	gcc	ccc	acc	tgt	agg	ggc	ccc	acc	ctc	ctc	cag	cac	gtc	938
180	Pro	Pro	Pro	Ala	Pro	Thr	Cys	Arg	Gly	Pro	Thr	Leu	Leu	Gln	His	Val	
181			255					260				265					
183	ttc	cct	gcc	tcc	cca	ggg	gcc	acc	ctg	gtg	ggg	ccc	cac	gga	cct	ctg	986
184	Phe	Pro	Ala	Ser	Pro	Gly	Ala	Thr	Leu	Val	Gly	Pro	His	Gly	Pro	Leu	
185		270					275				280						
187	gcc	tct	ggc	cag	cta	gca	gcc	ttc	cac	atc	gct	gcc	ccg	ctc	cct	gtc	1034
188	Ala	Ser	Gly	Gln	Leu	Ala	Ala	Phe	His	Ile	Ala	Ala	Pro	Leu	Pro	Val	
189	285				290				295					300			
191	act	gcc	aca	cgc	tgg	gac	ttc	gga	gac	ggc	tcc	gcc	gag	gtg	gat	gcc	1082
192	Thr	Ala	Thr	Arg	Trp	Asp	Phe	Gly	Asp	Gly	Ser	Ala	Glu	Val	Asp	Ala	
193				305				310					315				
195	gct	ggg	ccg	gct	gcc	tcg	cat	cgc	tat	gtg	ctg	cct	ggg	cgc	tat	cac	1130

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196	Ala	Gly	Pro	Ala	Ala	Ser	His	Arg	Tyr	Val	Leu	Pro	Gly	Arg	Tyr	His	
197				320					325					330			
199	gtg	acg	gcc	gtg	ctg	gcc	ctg	ggg	gcc	ggc	tca	gcc	ctg	ctg	ggg	aca	1178
200	Val	Thr	Ala	Val	Leu	Ala	Leu	Gly	Ala	Gly	Ser	Ala	Leu	Leu	Gly	Thr	
201			335					340					345				
203	gac	gtg	cag	gtg	gaa	gcg	gca	cct	gcc	gcc	ctg	gag	ctc	gtg	tgc	ccg	1226
204	Asp	Val	Gln	Val	Glu	Ala	Ala	Pro	Ala	Ala	Leu	Glu	Leu	Val	Cys	Pro	
205		350					355					360					
207	tcc	tcg	gtg	cag	agt	gac	gag	agc	ctt	gac	ctc	agc	atc	cag	aac	cgc	1274
208	Ser	Ser	Val	Gln	Ser	Asp	Glu	Ser	Leu	Asp	Leu	Ser	Ile	Gln	Asn	Arg	
209	365				370				375						380		
211	ggg	ggg	tca	ggc	ctg	gag	gcc	gcc	tac	agc	atc	gtg	gcc	ctg	ggc	gag	1322
212	Gly	Gly	Ser	Gly	Leu	Glu	Ala	Ala	Tyr	Ser	Ile	Val	Ala	Leu	Gly	Glu	
213				385					390				395				
215	gag	ccg	gcc	cga	gcg	gtg	cac	ccg	ctc	tgc	ccc	tcg	gac	acg	gag	atc	1370
216	Glu	Pro	Ala	Arg	Ala	Val	His	Pro	Leu	Cys	Pro	Ser	Asp	Thr	Glu	Ile	
217			400					405					410				
219	ttc	cct	ggc	aac	ggg	cac	tgc	tac	cgc	ctg	gtg	gtg	gag	aag	gcg	gcc	1418
220	Phe	Pro	Gly	Asn	Gly	His	Cys	Tyr	Arg	Leu	Val	Val	Glu	Lys	Ala	Ala	
221		415					420				425						
223	tgg	ctg	cag	gcg	cag	gag	cag	tgt	cag	gcc	tgg	gcc	ggg	gcc	gcc	ctg	1466
224	Trp	Leu	Gln	Ala	Gln	Glu	Gln	Cys	Gln	Ala	Trp	Ala	Gly	Ala	Ala	Leu	
225		430				435					440						
227	gca	atg	gtg	gac	agt	ccc	gcc	gtg	cag	cgc	ttc	ctg	gtc	tcc	cgg	gtc	1514
228	Ala	Met	Val	Asp	Ser	Pro	Ala	Val	Gln	Arg	Phe	Leu	Val	Ser	Arg	Val	
229	445				450				455						460		
231	acc	agg	agc	cta	gac	gtg	tgg	atc	ggc	ttc	tcg	act	gtg	cag	ggg	gtg	1562
232	Thr	Arg	Ser	Leu	Asp	Val	Trp	Ile	Gly	Phe	Ser	Thr	Val	Gln	Gly	Val	
233			465					470					475				
235	gag	gtg	ggc	cca	gcg	ccg	cag	ggc	gag	gcc	ttc	agc	ctg	gag	agc	tgc	1610
236	Glu	Val	Gly	Pro	Ala	Pro	Gln	Gly	Glu	Ala	Phe	Ser	Leu	Glu	Ser	Cys	
237		480					485						490				
239	cag	aac	tgg	ctg	ccc	ggg	gag	cca	cac	cca	gcc	aca	gcc	gag	cac	tgc	1658
240	Gln	Asn	Trp	Leu	Pro	Gly	Glu	Pro	His	Pro	Ala	Thr	Ala	Glu	His	Cys	
241		495					500				505						
243	gtc	cgg	ctc	ggg	ccc	acc	ggg	tgg	tgt	aac	acc	gac	ctg	tgc	tca	gcg	1706
244	Val	Arg	Leu	Gly	Pro	Thr	Gly	Trp	Cys	Asn	Thr	Asp	Leu	Cys	Ser	Ala	
245		510				515					520						
247	ccg	cac	agc	tac	gtc	tgc	gag	ctg	cag	ccc	gga	ggc	cca	gtg	cag	gat	1754
248	Pro	His	Ser	Tyr	Val	Cys	Glu	Leu	Gln	Pro	Gly	Gly	Pro	Val	Gln	Asp	
249	525				530				535						540		
251	gcc	gag	aac	ctc	ctc	gtg	gga	gcg	ccc	agt	ggg	gac	ctg	cag	gga	ccc	1802
252	Ala	Glu	Asn	Leu	Leu	Val	Gly	Ala	Pro	Ser	Gly	Asp	Leu	Gln	Gly	Pro	
253			545						550				555				
255	ctg	acg	cct	ctg	gca	cag	cag	gac	ggc	ctc	tca	gcc	ccg	cac	gag	ccc	1850
256	Leu	Thr	Pro	Leu	Ala	Gln	Gln	Asp	Gly	Leu	Ser	Ala	Pro	His	Glu	Pro	
257		560						565					570				
259	gtg	gag	gtc	atg	gta	ttc	ccg	ggc	ctg	cgt	ctg	agc	cgt	gaa	gcc	ttc	1898
260	Val	Glu	Val	Met	Val	Phe	Pro	Gly	Leu	Arg	Leu	Ser	Arg	Glu	Ala	Phe	

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261	575					580					585							
263	ctc	acc	acg	gcc	gaa	ttt	ggg	acc	cag	gag	ctc	cgg	cgg	ccc	gcc	cag	1946	
264	Leu	Thr	Thr	Ala	Glu	Phe	Gly	Thr	Gln	Glu	Leu	Arg	Arg	Pro	Ala	Gln		
265	590					595					600							
267	ctg	cgg	ctg	cag	gtg	tac	cgg	ctc	ctc	agc	aca	gca	ggg	acc	ccg	gag	1994	
268	Leu	Arg	Leu	Gln	Val	Tyr	Arg	Leu	Leu	Ser	Thr	Ala	Gly	Thr	Pro	Glu		
269	605					610					615					620		
271	aac	ggc	agc	gag	cct	gag	agc	agg	tcc	ccg	gac	aac	agg	acc	cag	ctg	2042	
272	Asn	Gly	Ser	Glu	Pro	Glu	Ser	Arg	Ser	Pro	Asp	Asn	Arg	Thr	Gln	Leu		
273	625					630					635							
275	gcc	ccc	gcg	tgc	atg	cca	ggg	gga	cgc	tgg	tgc	cct	gga	gcc	aac	atc	2090	
276	Ala	Pro	Ala	Cys	Met	Pro	Gly	Gly	Arg	Trp	Cys	Pro	Gly	Ala	Asn	Ile		
277	640					645					650							
279	tgc	ttg	ccg	ctg	gac	gcc	tct	tgc	cac	ccc	cag	gcc	tgc	gcc	aat	ggc	2138	
280	Cys	Leu	Pro	Leu	Asp	Ala	Ser	Cys	His	Pro	Gln	Ala	Cys	Ala	Asn	Gly		
281	655					660					665							
283	tgc	acg	tca	ggg	cca	ggg	cta	ccc	ggg	gcc	ccc	tat	gcg	cta	tgg	aga	2186	
284	Cys	Thr	Ser	Gly	Pro	Gly	Leu	Pro	Gly	Ala	Pro	Tyr	Ala	Leu	Trp	Arg		
285	670					675					680							
287	gag	ttc	ctc	ttc	tcc	gtt	gcc	gcg	ggg	ccc	ccc	gcg	cag	tac	tcg	gtc	2234	
288	Glu	Phe	Leu	Phe	Ser	Val	Ala	Ala	Gly	Pro	Pro	Ala	Gln	Tyr	Ser	Val		
289	685					690					695					700		
291	acc	ctc	cac	ggc	cag	gat	gtc	ctc	atg	ctc	cct	ggc	gac	ctc	gtt	ggc	2282	
292	Thr	Leu	His	Gly	Gln	Asp	Val	Leu	Met	Leu	Pro	Gly	Asp	Leu	Val	Gly		
293	705					710					715							
295	ttg	cag	cac	gac	gct	ggc	cct	ggc	gcc	ctc	ctg	cac	tgc	tcg	ccg	gct	2330	
296	Leu	Gln	His	Asp	Ala	Gly	Pro	Gly	Ala	Leu	Leu	His	Cys	Ser	Pro	Ala		
297	720					725					730							
299	ccc	ggc	cac	cct	ggc	ccc	cag	gcc	ccg	tac	ctc	tcc	gcc	aac	gcc	tcg	2378	
300	Pro	Gly	His	Pro	Gly	Pro	Gln	Ala	Pro	Tyr	Leu	Ser	Ala	Asn	Ala	Ser		
301	735					740					745							
303	tca	tgg	ctg	ccc	cac	ttg	cca	gcc	cag	ctg	gag	ggc	act	tgg	gcc	tgc	2426	
304	Ser	Trp	Leu	Pro	His	Leu	Pro	Ala	Gln	Leu	Glu	Gly	Thr	Trp	Ala	Cys		
305	750					755					760							
307	cct	gcc	tgt	gcc	ctg	cgg	ctg	ctt	gca	gcc	acg	gaa	cag	ctc	acc	gtg	2474	
308	Pro	Ala	Cys	Ala	Leu	Arg	Leu	Leu	Ala	Ala	Thr	Glu	Gln	Leu	Thr	Val		
309	765					770					775					780		
311	ctg	ctg	ggc	ttg	agg	ccc	aac	cct	gga	ctg	cgg	atg	cct	ggg	cgc	tat	2522	
312	Leu	Leu	Gly	Leu	Arg	Pro	Asn	Pro	Gly	Leu	Arg	Met	Pro	Gly	Arg	Tyr		
313	785					790					795							
315	gag	gtc	cgg	gca	gag	gtg	ggc	aat	ggc	gtg	tcc	agg	cac	aac	ctc	tcc	2570	
316	Glu	Val	Arg	Ala	Glu	Val	Gly	Asn	Gly	Val	Ser	Arg	His	Asn	Leu</			

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date